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PATENT

App. No. 09/438,185

Response to Office communication dated 09/03/2003

Office communication of July 8, 2003

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Replacement Pages to the Specification:

Please replace pages 37 and 123 with the following replacement pages, together with annotated sheets showing changes in highlights. The replacement pages and annotated pages are attached to this amendment.

Attachment: Replacement Sheets
Annotated Sheets Showing Changes

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tRNAs

<u>tRNA #</u>	<u>Begin</u>	<u>End</u>	<u>Type</u>	<u>Codon</u>
1	89657	89728	Thr	GGT
2	90998	91070	Trp	CCA
3	199301	199229	Met	CAT
4	199390	199317	Met	CAT
5	296075	296147	Val	TAC
6	296151	296224	Asp	GTC
7	409848	409922	Pro	TGG
8	462141	462214	Arg	CCT
9	672236	672318	Leu	CAA
10	677264	677337	Arg	TCG
11	739403	739486	Leu	CAG
12	781610	781680	Gly	TCC
13	784822	784896	Glu	TTC
14	784922	784994	Lys	TTT
15	836119	836191	Ala	GGC
16	843926	843999	Pro	GGG
17	877400	877473	Arg	ACG
18	1085605	1085676	Gln	TTG
19	1142034	1142118	Ser	TGA
20	1175863	1175944	Leu	TAG
21	1230028	1229942	Ser	CGA
22	1137462	1137389	Val	GAC
23	1030603	1030533	Cys	GCA
24	1000022	999949	His	GTG
25	961607	961536	Gly	GCC
26	807413	807341	Arg	TCT
27	786780	786708	Thr	CGT
28	715971	715889	Leu	TAA
29	708441	708354	Ser	GCT
30	680259	680178	Leu	GAG
	631445	631373	Phe	GAA
32	626987	626901	Ser	GGA
33	293477	293405	Thr	TGT
34	293399	293317	Tyr	GTA
35	269142	269070	Ala	TGC
36	269065	268992	Ile	GAT
37	1643089	164318	Asn	GTT
38	87522	87450	Met	CAT



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TABLE 2

Gene #	From	To	Strand	Gene Function (C. Trachomatis Ortholog in parenthesis)
CPn0001	282	4	R	CT001 hypothetical protein
CPn0002	573	875	F	gatC-Glu-tRNA Gln Amidotransferase (C subunit) - (CT002)
CPn0003	895	2370	F	gatA-Glu tRNA Gln Amidotransferase-(CT003)
CPn0004	2370	3833	F	gatB-(Pet 112) Glu tRNA Gln Amidotransferase (B Subunit)
CPn005	4127	6892	F	pmp_1-Polymorphic Outer Membrane Protein G Family
CPn006	7293	7141	R	
CPn007	7605	10496	F	
CPn008	10975	11685	F	
CPn009	11815	13119	F	
CPn0010	13435	14325	F	
CPn0010	14379	15746	F	frame-shift with 0010
CPn0011	15892	16614	F	
CPn0012	16644	18212	F	
CPn0013	18584	21106	F	pmp_2-Polymorphic Outer Membrane Protein G Family
CPn0014	21392	21922	F	pmp_3-Polymorphic Outer Membrane Protein G Family
CPn0015	21835	24174	F	pmp_3-PMP_3 (frame-shift with 0014)
CPn0016	24416	26188	F	pmp_4-Polymorphic Outer Membrane Protein G Family
CPn0017	26094	27170	F	pmp_4-PMP_4 (frame-shift with 0016)
CPn0018	27522	29003	F	pmp_5-Polymorphic Outer Membrane Protein G Family
CPn0019	29007	30356	F	pmp_5-PMP_5 (frame-shift with 0018)
CPn0020	32687	30603	R	Predicted OMP [leader (14) peptide: outer membrane] - (CT351)
CPn0021	34410	32707	R	Predicted OMP [leader (19) peptide] - (CT350)
CPn0022	34982	34395	R	maf-(CT349)
CPn0023	36603	35014	R	yjjK/alr-ABC Transporter Protein ATPase-(CT348)
CPn0024	37596	36661	R	xerC-Integrase/recombinase-(CT347)
CPn0025	38604	37684	R	elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346)
CPn0026	39625	38762	R	CT345 hypothetical protein-(CT345)
CPn0027	42234	39778	R	lon-Lon ATP-dependent Protease-(CT344)
CPn0028	43325	42543	R	
CPn0029	43755	43390	R	
CPn0030	43891	44529	F	gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343)
CPn0031	44711	44884	F	rs21-S21 Ribosomal Protein-(CT342)
CPn0032	44923	46098	F	dnaJ-Heat Shock Protein J-(CT341)
CPn0033	46138	48171	F	pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & ___ Fusion-(CT340)
CPn0034	49457	48210	R	
CPn0035	51029	49569	R	CT339 hypothetical protein
CPn0036	51002	51796	F	CT338 hypothetical protein
CPn0037	51792	52115	F	ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
CPn0038	52119	53831	F	ptsI-PTS PEP Phosphotransferase-(CT336)
CPn0039	54250	53963	R	ybaB-(CT335)



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CPn009	11815	13119	F	
CPn0010	13435	14325	F	
CPn0010	14379	15746	F	frame-shift with 0010
CPn0011	15892	16614	F	
CPn0012	16644	18212	F	
CPn0013	18584	21106	F	pmp_2-Polymorphic Outer Membrane Protein G Family
CPn0014	21392	21922	F	pmp_3-Polymorphic Outer Membrane Protein G Family
CPn0015	21835	24174	F	pmp_3-PMP_3 (frame-shift with 0014)
CPn0016	24416	26188	F	pmp_4-Polymorphic Outer Membrane Protein G Family
CPn0017	26094	27170	F	pmp_4-PMP_4 (frame-shift with 0016)
CPn0018	27522	29003	F	pmp_5-Polymorphic Outer Membrane Protein G Family
CPn0019	29007	30356	F	pmp_5-PMP_5 (frame-shift with 0018)
CPn0020	32687	30603	R	Predicted OMP [leader (14) peptide: outer membrane] - (CT351)
CPn0021	34410	32707	R	Predicted OMP [leader (19) peptide] - (CT350)
CPn0022	34982	34395	R	maf-(CT349)
CPn0023	36603	35014	R	yjK/alr-ABC Transporter Protein ATPase-(CT348)
CPn0024	37596	36661	R	xerC-Integrase/recombinase-(CT347)
CPn0025	38604	37684	R	elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346)
CPn0026	39625	38762	R	CT345 hypothetical protein-(CT345)
CPn0027	42234	39778	R	lon-Lon ATP-dependent Protease-(CT344)
CPn0028	43325	42543	R	
CPn0029	43755	43390	R	
CPn0030	43891	44529	F	gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343)
CPn0031	44711	44884	F	rs21-S21 Ribosomal Protein-(CT342)
CPn0032	44923	46098	F	dnaJ-Heat Shock Protein J-(CT341)
CPn0033	46138	48171	F	pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & ___ Fusion-(CT340)
CPn0034	49457	48210	R	
CPn0035	51029	49569	R	CT339 hypothetical protein
CPn0036	51002	51796	F	CT338 hypothetical protein
CPn0037	51792	52115	F	ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
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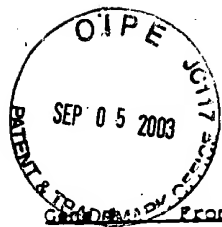


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CPn0039	54250	53963	R	ybaB-(CT335)
CPn0040	55643	54318	R	dnaX_1-DNA Pol III Gamma and Tau_1-(CT334)
CPn0041	55996	57342	F	
CPn0042	57403	58182	F	
CPn0043	58447	60372	F	
CPn0044	60419	60778	F	
CPn0045	61069	62790	F	
CPn0046	62790	63263	F	
CPn0047	63455	63652	F	
CPn0048	63687	65801	F	*yqfP-Bs conserved hypothetical IM protein
CPn0049	66296	65817	R	
CPn0050	66813	66499	R	
CPn0051	66833	67111	F	
CPn0052	68005	67304	R	hemC-Porphobilinogen Deaminase-(CT299)
CPn0053	69344	67986	R	sms-Sms Protein-(CT298)
CPn0054	70023	69313	R	rnc-Ribonuclease III-(CT297)
CPn0055	70129	70590	F	CT296 hypothetical protein
CPn0056	70953	72746	F	mrsA-Phosphomannomutase-(CT295)
CPn0057	72934	73554	F	sodM-Superoxide Dismutase (Mn)-(CT294)
CPn0058	73639	74562	F	accD-AcCoA Carboxylase/Transferase Beta-(CT293)
CPn0059	74616	75050	F	dut-dUTP Nucleotidohydrolase-(CT292)
CPn0060	75055	75528	F	ptsN_1-PTS IIA Protein-(CT291)
CPn0061	75534	76208	F	ptsN_2-PTS IIA Protein + HTH DNA-Binding Domain-(CT290)
CPn0062	76308	77690	F	CT289 hypothetical protein
CPn0063	78112	78267	F	
CPn0064	78346	78576	F	
CPn0065	78924	80651	F	CT288 hypothetical protein
CPn0066	80925	82655	F	

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